Shown is the 3'UTR of the human IL1B sequence from accession number M15330.
* Represents the stop codon.

*AGAGAGCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAG
GGCTGGCAGAAAGGGAACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGAC
TTTCCTGTTGTCTACACCAATGCCCAACTGCCTGCCTTAGGGTAGTGCTAA
GAGGATCTCCTGTCCATCAGCCAGGACAGTCAGCTCTCTCCTTTCAGGGCC
AATCCCCCAGCCCTTTTGTTGAGCCAGGCCTCTCTCACCTCTCCTACTCACT
TAAAGCCCGCCTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCCTC
TGTCATTCGCTCCCCACATTCTGATGAGCAACCGCTTCCCCT***ATTTATTTATT***
TATTTGTTTGTTTATTCATTGGTCTA***ATTTA***TTCAAAGGGGGCAAG
AAGTAGCAGTGTCTGTAAAAGAGCCTAGTTTTTAATAGCTATGGAATCAAT
TCAATTTGGACTGGTGTGCTCTCTTTAAATCAAGTCCTTTAATTAAGACTG
AAAATATATAAGCTCAGATT***ATTTA***AATGGGAAT***ATTTA***TAAATGAGCAAA
TATCATACTGTTCAATGGTTCTGAAATAACTTCTCTGAAG

FIGURE 1

ATGGCTTCCCTATTTATTTATTTATTTGTTTGTCCAACCT
GGATACCGAAGGGATAAATAAATAAATAAACAAACAGGTT

FIGURE 2

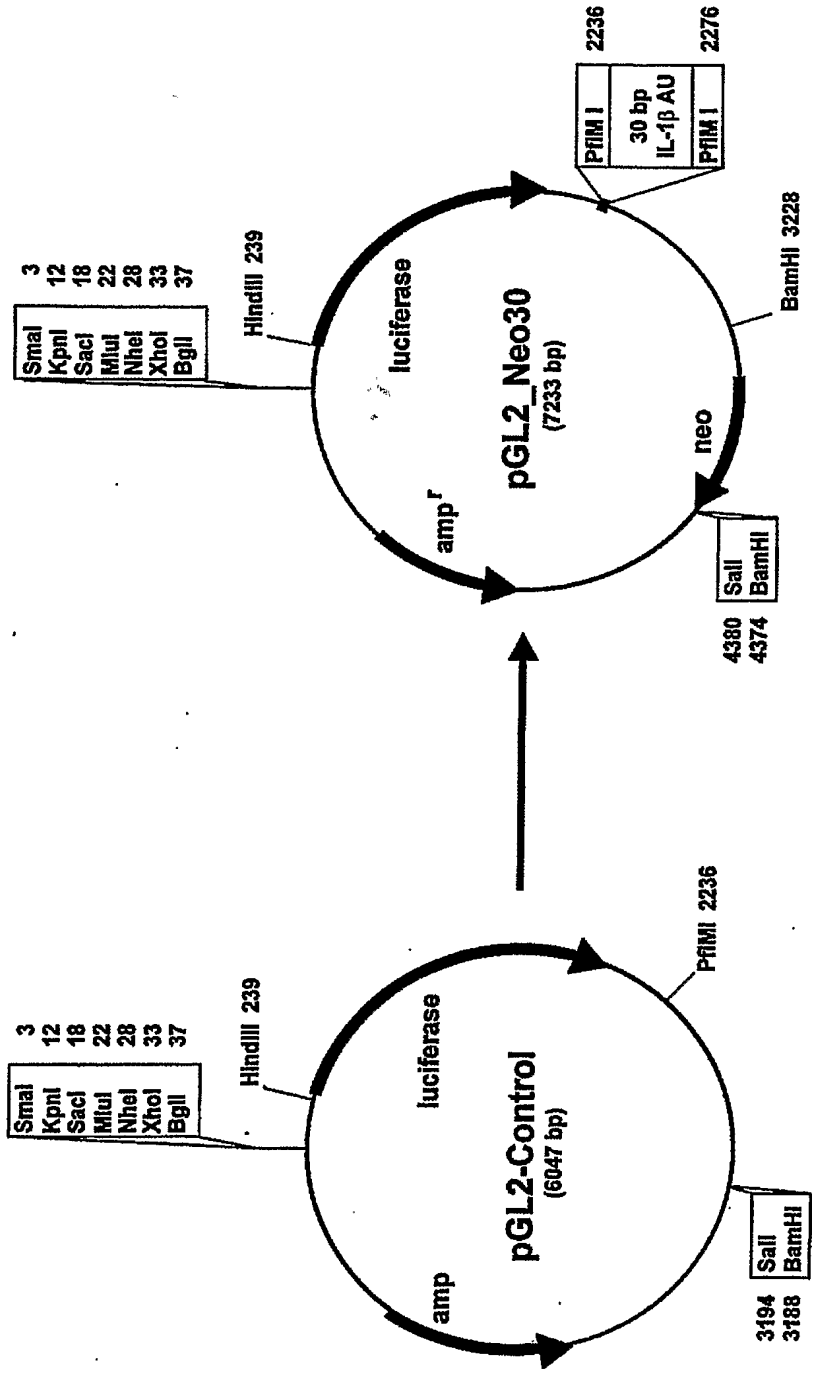

pGL2-Control
(6047 bp)
luciferase
amp
HindIII 239
3
12
18
22
28
33
37
SmaI
KpnI
SacI
MluI
NheI
XhoI
BglII
PflMI 2236
SalI
BamHI
3194
3188
pGL2_Neo30
(7233 bp)
luciferase
amp r
neo
HindIII 239
PflMI 2236
30 bp
IL-1β AU
PflMI 2276
BamHI 3228
SalI
BamHI
4380
4374

FIGURE 3A

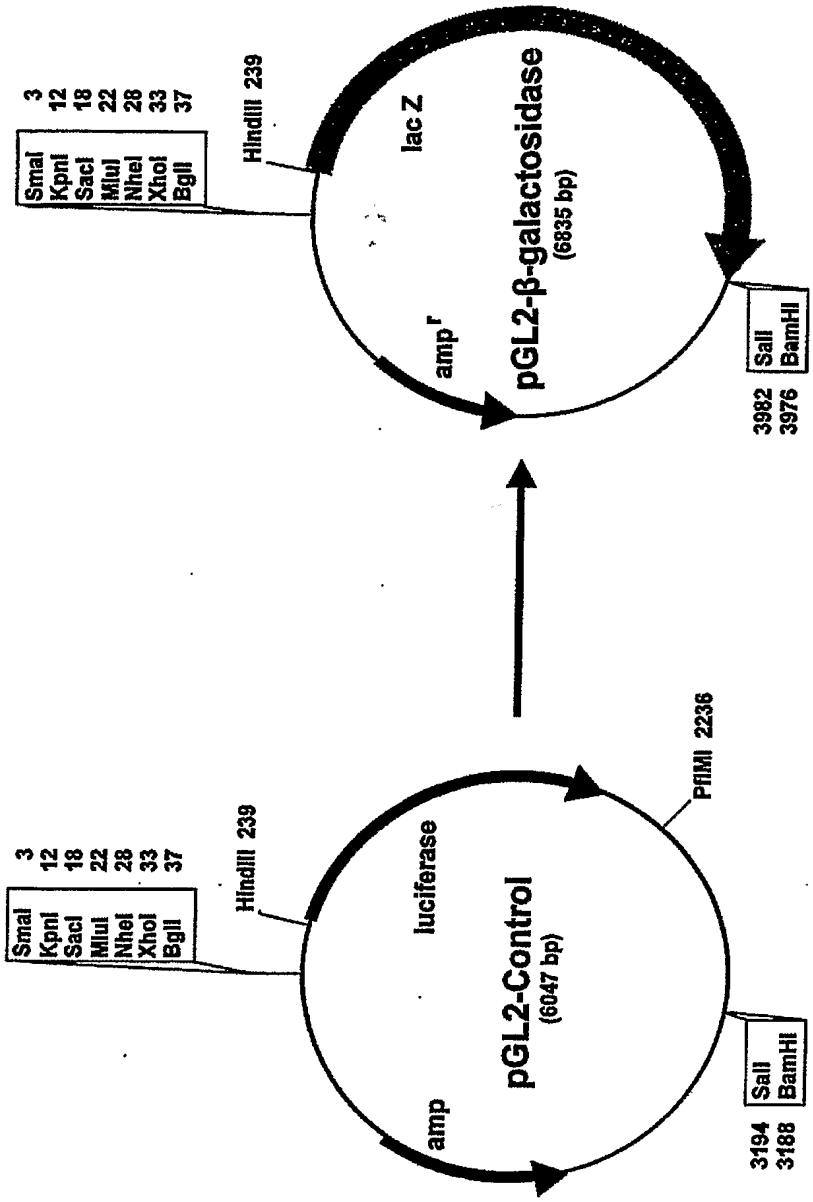

pGL2-β-galactosidase
(6835 bp)
lac Z
amp r
HindIII 239
3
12
18
22
28
33
37
SmaI
KpnI
SacI
MluI
NheI
XhoI
BglI
SalI
BamHI
3982
3976
pGL2-Control
(6047 bp)
luciferase
amp
HindIII 239
PflMI 2236
3194
3188

FIGURE 3B

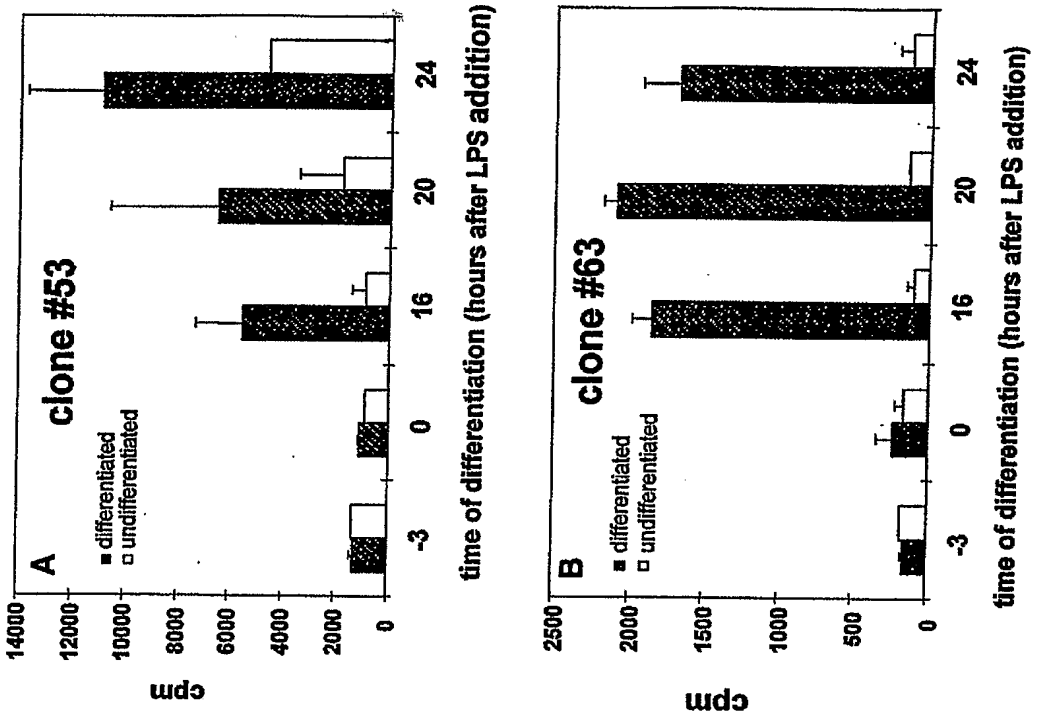

A
clone #53
differentiated
undifferentiated
cpm
14000
12000
10000
8000
6000
4000
2000
0
-3
0
16
20
24
time of differentiation (hours after LPS addition)
B
clone #63
differentiated
undifferentiated
cpm
2500
2000
1500
1000
500
0
-3
0
16
20
24
time of differentiation (hours after LPS addition)

FIGURE 4

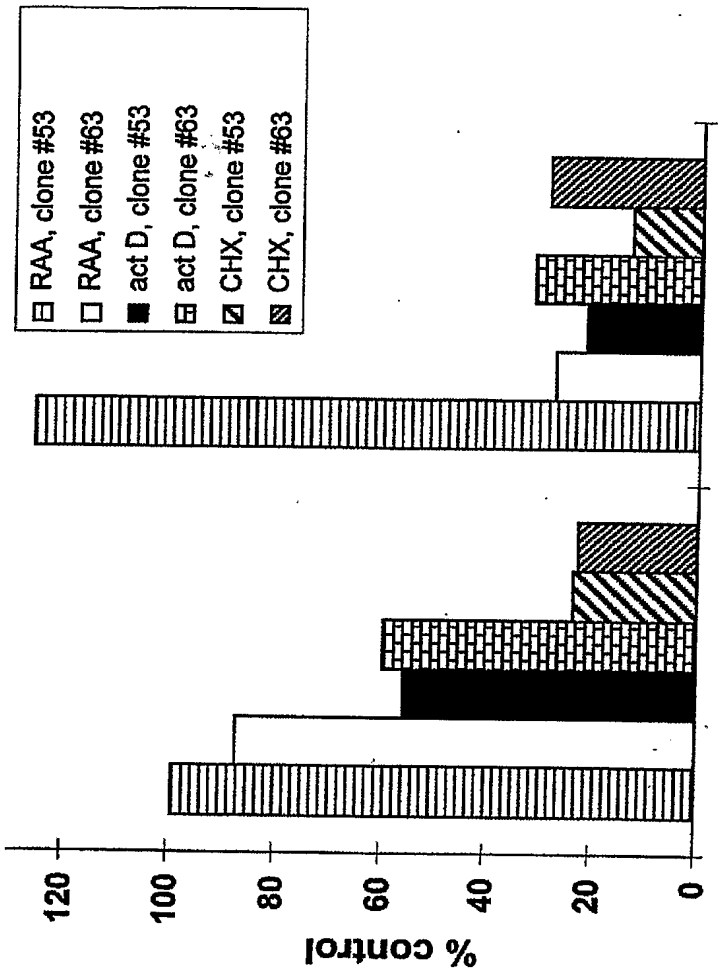

RAA, clone #53
RAA, clone #63
act D, clone #53
act D, clone #63
CHX, clone #53
CHX, clone #63
% control
120
100
80
60
40
20
0
4
8
hours after addition of compounds

FIGURE 5

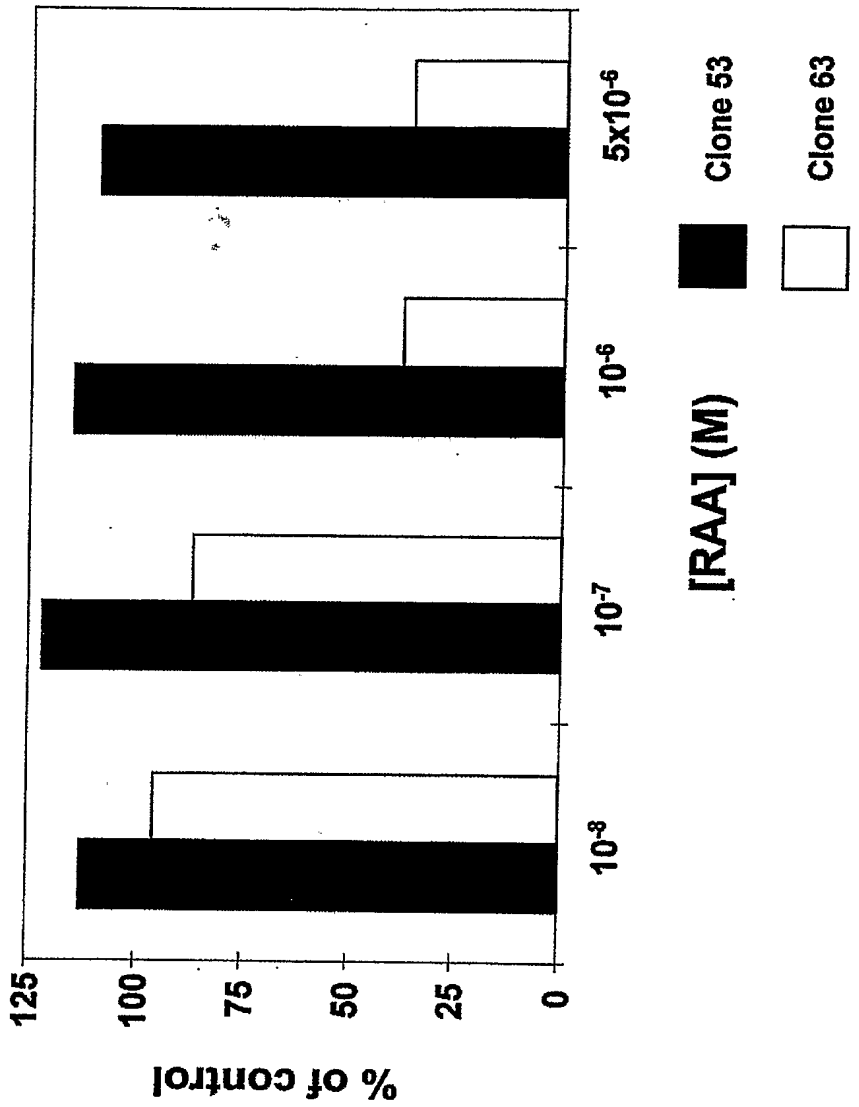

% of control
125
100
75
50
25
0
10-8
10-7
10-6
5x10-6
[RAA] (M)
Clone 53
Clone 63

FIGURE 6

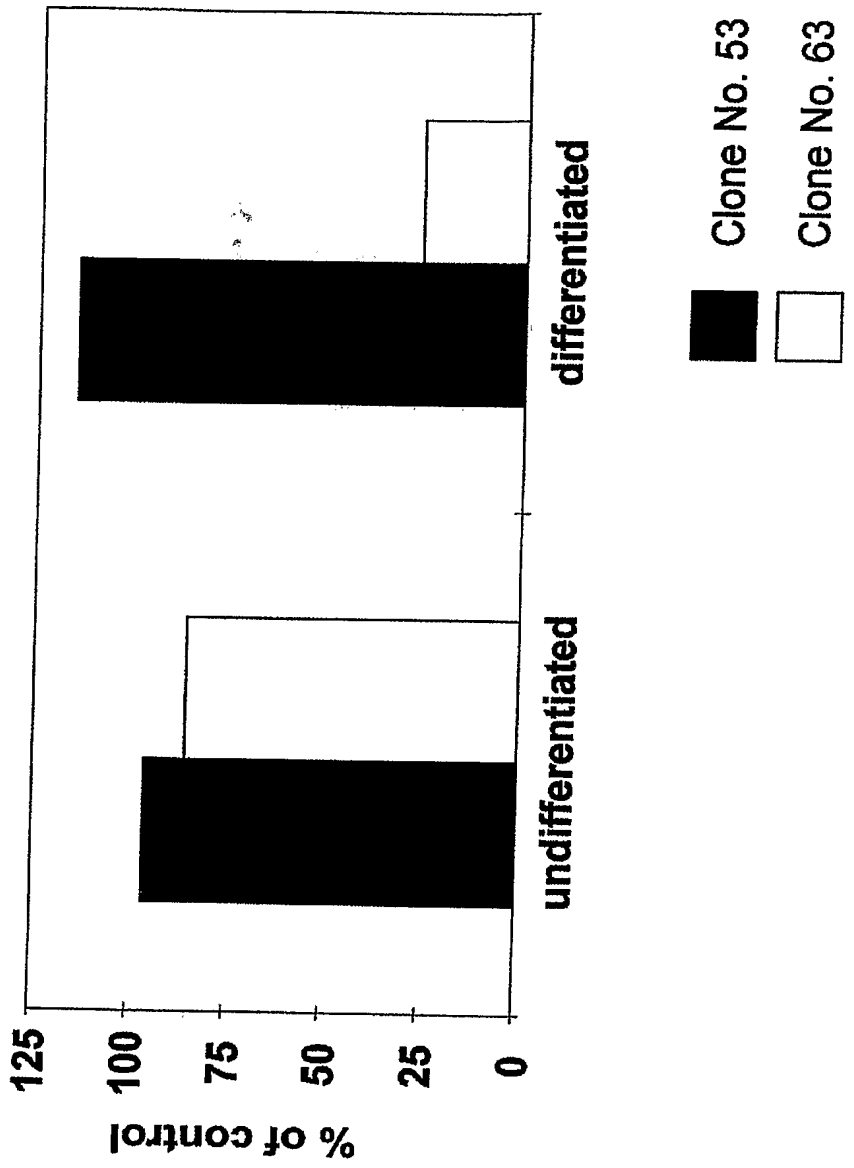

Clone No. 53
Clone No. 63
differentiated
undifferentiated
% of control
125
100
75
50
25
0

FIGURE 7

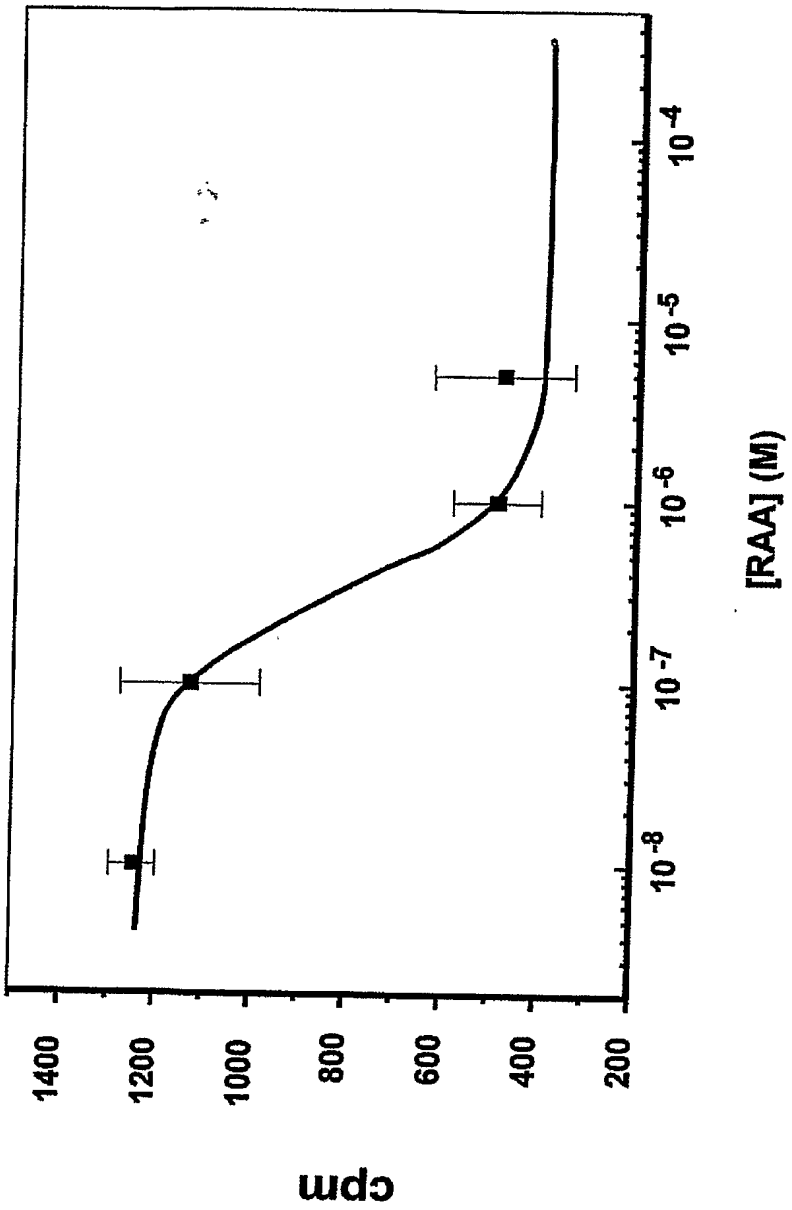


FIGURE 8

APP construct:

AUUUA {Bold/Underline}
potential polyA signal sequence {Bold/Italics}
Restriction Sites {Bold}

	NotI
1	GCGGCCGCCA CAGCAGCCTC TGAAGTTGGA CAGCAAAACC ATTGCTTCAC TACCCATCGG TGTCCATTTA TAGAATAATG TGGGAAGAAA CAAACCCGTT
101	TTATGATTTA CTCATTATCG CCTTTTGACA GCTGTGCTGT AACACAAGTA GATGCCTGAA CTTGAATTAA TCCACACATC AGTAATGTAT TCTATCTCTC
201	TTTACATTTT GGTCTCTATA CTACATTATT AATGGGTTTT GTGTACTGTA AAGAATTTAG CTGTATCAAA CTAGTGCATG AATAGATTCT CTCCTGATTA
301	TTTATCACAT AGCCCCTTAG CCAGTTGTAT ATTATTCTTG TGGTTTGTGA CCCAATTAAG TCCTACTTTA CATATGCTTT AAGAATCGAT GGGGGATGCT
401	TCATGTGAAC GTGGGAGTTC AGCTGCTTCT CTTGCCTAAG TATTCCTTTC CTGATCACTA TGCATTTTAA AGTTAAACAT TTTTAAGTAT TTCAGATGCT
501	TTAGAGAGAT TTTTTTTTCC ATGACTGCAT TTTACTGTAC AGATTGCTGC TTCTGCTATA TTTGTGATAT AGGAATTAAG AGGATACACA CGTTTGTTTC
601	TTCGTGCCTG TTTTATGTGC ACACATTAGG CATTGAGACT TCAAGCTTTT CTTTTTTTGT CCACGTATCT TTGGGTCTTT GATAAAGAAA AGAATCCCTG
701	TTCATTGTAA GCACTTTTAC GGGGCGGGTG GGGAGGGGTG CTCTGCTGGT CTTCAATTAC CAAGAATTCT CCAAAACAAT TTTCTGCAGG ATGATTGTAC
801	AGAATCATTG CTTATGACAT GATCGCTTTC TACACTGTAT TACATAAATA AATTAAATAA AATAACCCCG GGCAAGACTT TTCTTTGAAG GATGACTACA
901	GACATTAAAT AATCGAAGTA ATTTTGGGTG GGGAGAAGAG GCAGATTCAA TTTTCTTTAA CCAGTCTGAA GTTTCATTTA TGATACAAAA GAAGATGAAA
1001	ATGGAAGTGG CAATATAAGG GGATGAGGAA GGCATGCCTG GACAAACCCT TCTTTTAAGA TGTGTCTTCA ATTTGTATAA AATGGTGTTT TCATGTAGCG
1101	GCCGC
	NotI

FIGURE 9

Length: 1105 bp

NotI

1 GCGGCCGCTG AAGTCAACAT GCCTGCCCCA AACAAATATG CAAAGGTTC ACTAAAGCAG TAGAAATAAT ATGCATTGTC AGTGATGTAC CATGAAACAA

101 AGCTGCAGGC TGTTTAAGAA AAAATAACAC ACATATAAAC ATCACACACA CAGACAGACA CACACACACA CAACAATTAA CAGTCTTCAG GCAAAACGTC

201 GAATCAGCTA TTTACTGCCA AAGGGAAATA TCATTTATTT TTTACATTAT TAAGAAAAAA AGATTTATTT ATTTAAGACA GTCCCATCAA AACTCCTGTC

301 TTTGGAAATC CGACCACTAA TTGCCAAGCA CCGCTTCGTG TGGCTCCACC TGGATGTTCT GTGCCTGTAA ACATAGATTC GCTTTCCATG TTGTTGGCCG

401 GATCACCATC TGAAGAGCAG ACGGATGGAA AAAGGACCTG ATCATTGGGG AAGCTGGCTT TCTGGCTGCT GGAGGCTGGG GAGAAGGTGT TCATTCACTT

501 GCATTTCTTT GCCCTGGGGG CTGTGATATT AACAGAGGGA GGGTTCCTGT GGGGGGAAGT CCATGCCTCC CTGGCCTGAA GAAGAGACTC TTTGCATATG

601 ACTCACATGA TGCATACCTG GTGGGAGGAA AAGAGTTGGG AACTTCAGAT GGACCTAGTA CCCACTGAGA TTTCCACGCC GAAGGACAGC GATGGGAAAA

701 ATGCCCTTAA ATCATAGGAA AGTATTTTTT TAAGCTACCA ATTGTGCCGA GAAAAGCATT TTAGCAATTT ATACAATATC ATCCAGTACC TTAAGCCCTG

801 ATTGTGTATA TTCATATATT TTGGATACGC ACCCCCCAAC TCCCAATACT GGCTCTGTCT GAGTAAGAAA CAGAATCCTC TGGAACTTGA GGAAGTGCGG

901 CCGC

NotI

Length: 904 bp

FIGURE 10

stop codon {Bold/Italics/Underline}
bcl-2α-short construct:
AUUUA {Bold/Underline}
Restriction Sites {Bold}
NotI
1 GCGGCCGCTG AAGTCAACAT GCCTGCCCCA AACAAATATG CAAAAGGTTC
51 ACTAAAGCAG TAGAAATAAT ATGCATTGTC AGTGATGTAC CATGAAACAA
101 AGCTGCAGGC TGTTTAAGAA AAAATAACAC ACATATAAAC ATCACACACA
151 CAGACAGACA CACACACACA CAACAATTAA CAGTCTTCAG GCAAAACGTC
201 GAATCAGCTA TTTACTGCCA AAGGGAAATA TCATTTATTT TTTACATTAT
251 TAAGAAAAAA AGATTTATTT ATTTAAGACA GTCCCATCAA AACTCCTGTC
301 TTTGGAAATC CGACCACTAA TTGCCAAGCA CCGCTTCGTG TGGCTCCACC
351 TGGATGTTCT GTGCCTGTAA ACATAGATTC GCTTTCCATG TTGTTGGCCG
401 GATCACCATC TGAAGAGCAG ACGGATGGAA AAAGGACCTG ATCATTGGGG
451 AAGCTGGCTT TCTGGCTGCT GGAGGCTGGG GAGAAGGTGT TCATTCACTT
501 GCATTTCTTT GCCCTGGGGG CTGTGATATT AACAGAGGGA GGGTTCCTGT
551 GGGGGGAAGT CCATGCCTCC CTGGCCTGAA GAAGACACTC TTTGCATATG
601 ACTCACATGA TGCATACCTG GTGGGAGGAA AAGAGTTGGG AACTTCAGAT
651 GGACCTAGTA CCCACTGAGA TTTCCACGCC GAAGGACAGC GATGGGAAAA
701 ATGCGGCCGC
NotI
Length: 710 bp

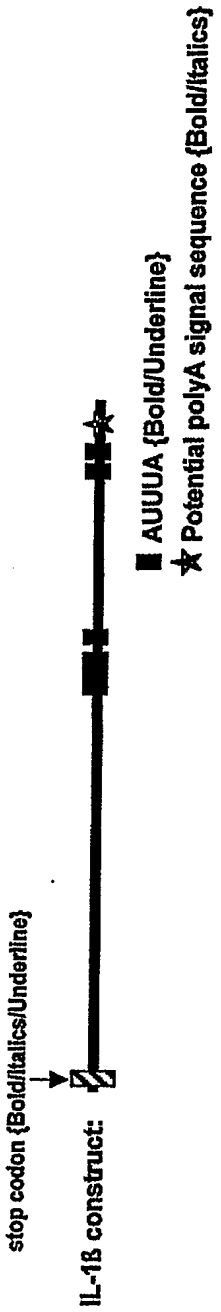
FIGURE 11

stop codon {Bold/Italics/Underline}
c-myc construct:
CRD
AUUUA {Bold/Underline}
CRD:
potential polyA signal sequence {Bold/Italics}
coding region instability determinant {Underline}
Restriction Sites {Bold}
NotI
1 GCGGCCGCTC GGAGCTTTTT TGCCCTGCGT GACCAGATCC CGGAGTTGGA
51 AAACAATGAA AAGGCCCCCA AGGTAGTTAT CCTTAAAAAA GCCACAGCAT
101 ACATCCTGTC CGTCCAAGCA GAGGAGCAAA AGCTCATTTC TGAAGAGGAC
151 TTGTTGCGGA AACGACGAGA ACAGTTGAAA CACAAACTTG AACAGCTACG
201 GAACTCTTGT GCGTAAGGAA AAGTAAGGAA AACGATTCCT TCTGACAGAA
251 ATGTCCTGAG CAATCACCTA TGAACTTGTT TCAAATGCAT GATCAAATGC
301 AACCTCACAA CCTTGGCTGA GTCTTGAGAC TGAAAGATTT AGCCATAATG
351 TAAACTGCCT CAAATTGGAC TTTGGGCATA AAAGAACTTT TTTATGCTTA
401 CCATCTTTTT TTTTCTTTA ACAGATTTGT ATTTAAGAAT TGTTTTTAAA
451 AAATTTTAAG ATTTACACAA TGTTTCTCTG TAAATATTGC CATTAAATGT
501 AAATAACTTT AATAAAACGT TTATAGCAGT TACACAGAAT TTCAATCCTA
551 GTATATAGTA CCTAGTATTA TAGGTACTAT AAACCCTAAT TTTTTTATT
601 TAAGTACATT TTGCTTTTTA AAGTTGATTT TTTTCTATTG TTTTTAGAAA
651 AAATAAAATA ACTGGCAAAT ATATCATTGA GCCATATG
NdeI
Length: 688 bp

FIGURE 12

stop codon {Bold/Italics/Underline}
TNF-α construct:
AUUUA {Bold/Underline}
Potential polyA signal sequence {Bold/Italics}
Restriction Sites {Bold}
NotI
1 GCGGCCGCTG AGGAGGACGA ACATCCAACC TTCCCAAACG CCTCCCCTGC CCCAATCCCT
61 TTATTACCCC CTCCTTCAGA CACCCTCAAC CTCTTCTGGC TCAAAAAGAG AATTGGGGGC
121 TTAGGGTCGG AACCCAAGCT TAGAACTTTA AGCAACAAGA CCACCACTTC GAAACCTGGG
181 ATTCAGGAAT GTGTGGCCTG CACAGTGAAG TGCTGGCAAC CACTAAGAAT TCAAACTGGG
241 GCCTCCAGAA CTCACTGGGG CCTACAGCTT TGATCCCTGA CATCTGGAAT CTGGAGACCA
301 GGGAGCCTTT GGTTCTGGCC AGAATGCTGC AGGACTTGAG AAGACCTCAC CTAGAAATTG
361 ACACAAGTGG ACCTTAGGCC TTCCTCTCTC CAGATGTTTC CAGACTTCCT TGAGACACGG
421 AGCCCAGCCC TCCCCATGGA GCCAGCTCCC TCTATTTATG TTTGCACTTG TGATTATTTA
481 TTATTTATTT ATTATTTATT TATTTACAGA TGAATGTATT TATTTGGGAG ACCGGGGTAT
541 CCTGGGGGAC CCAATGTAGG AGCTGCCTTG GCTCAGACAT GTTTTCCGTG AAAACGGAGC
601 TGAACAATAG GCTGTTCCCA TGTAGCCCCC TGGCCTCTGT GCCTTCTTTT GATTATGTTT
661 TTTAAAATAT TTATCTGATT AAGTTGTCTA AACAATGCTG ATTTGGTGAC CAACTGTCAC
721 TCATTGCTGA GCCTCTGCTC CCCAGGGGAG TTGTGTCTGT AATCGCCCTA CTATTCAGTG
781 GCGAGAAATA AAGTTTGCTT CATATG
NdeI
Length: 806 bp

FIGURE 13



■ AUUUA {Bold/Underline}
★ Potential polyA signal sequence {Bold/Italics}
Restriction Sites {Bold}

NotI

```
   1 GCGGCCGCTA AAGAGAGCTG TACCCAGAGA GTCCTGTGCT GAATGTGGAC
  51 TCAATCCCTA GGCTGGCAG AAAGGGAACA GAAAGTTTT TGAGTACGGC
 101 TATAGCCTGG ACTTTCCTGT TGTCTACACC AATGCCCAAC TGCCTGCCTT
 151 AGGGTAGTGC TAAGAGGATC TCCTGTCCAT CAGCCAGGAC AGTCAGCTCT
 201 CTCCTTTCAG GGCCAATCCC CAGCCCTTTT GTTGAGCCAG GCCTCTCTCA
 251 CCTCTCCTAC TCACTTAAAG CCCGCCTGAC AGAAACCACG GCCACATTTG
 301 GTTCTAAGAA ACCCTCTGTC ATTCGCTCCC ACATTCTGAT GAGCAACCGC
 351 TTCCCTATTT ATTTATTTAT TTGTTTGTTT GTTTTATTCA TTGGTCTAAT
 401 TTATTCAAAG GGGGCAAGAA GTAGCAGTGT CTGTAAAAGA GCCTAGTTTT
 451 TAATAGCTAT GGAATCAATT CAATTTGGAC TGGTGTGCTC TCTTTAAATC
 501 AAGTCCTTTA ATTAAGACTG AAAATATATA AGCTCAGATT ATTTAAATGG
 551 GAATATTTAT AAATGAGCAA ATATCATACT GTTCAATGGT TCTGAAATAA
 601 ACTTCACCAT ATG
```

NdeI

Length: 613 bp

FIGURE 14

Length: 1101 bp

FIGURE 15

VEGF 3'UTR hypoxia domain construct:

AUUUA {Bold/Underline}
Restriction Sites {Bold}

NotI

1 **GCGGCCGCAT** TCCTGTAGAC ACACCCACCC ACATACATAC **ATTTA**TATAT

51 ATATATATTA TATATATATA AAAATAAATA TCTCTATTTT ATATATATAA

101 AATATATATA TTCTTTTTTT AAATTAACAG TGCTAATGTT ATTGGTGTCT

151 TCACTGGATG **AACATATG**

NdeI

Length: 168 bp

FIGURE 16

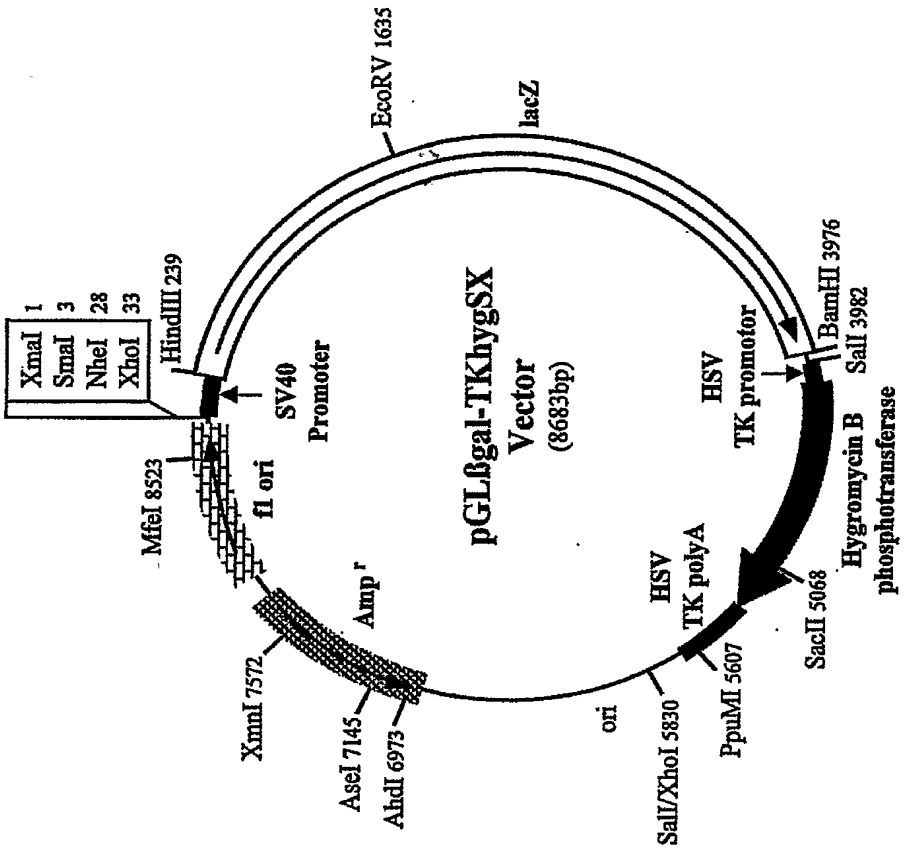

pGLßgal-TKhygSX
Vector
(8683bp)
lacZ
EcoRV 1635
BamHI 3976
SalI 3982
HSV
TK promotor
Hygromycin B
phosphotransferase
SacII 5068
HSV
TK polyA
PpuMI 5607
SalI/XhoI 5830
ori
AhdI 6973
AseI 7145
XmnI 7572
Ampr
f1 ori
MfeI 8523
SV40
Promoter
HindIII 239
XmaI 1
SmaI 3
NheI 28
XhoI 33

FIGURE 17